

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/533,103  
Source: 17600  
Date Processed by STIC: 8/21/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

### Raw Sequence Listing Error Summary

### SUGGESTED CORRECTION

SERIAL NUMBER: 10533, 103

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1 \_\_\_\_\_ Wrapped Nucleic  
Amino Acids The number/text at the end of each amino acid line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 \_\_\_\_\_ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 \_\_\_\_\_ Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 \_\_\_\_\_ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 \_\_\_\_\_ Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 \_\_\_\_\_ PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 \_\_\_\_\_ Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 \_\_\_\_\_ Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 \_\_\_\_\_ Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 \_\_\_\_\_ Invalid <213>  
Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 \_\_\_\_\_ Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 \_\_\_\_\_ PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 \_\_\_\_\_ Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 08/21/2006

PATENT APPLICATION: US/10/533,103

TIME: 10:18:36

Input Set : F:\3514 115 ST25.txt

Output Set: N:\CRF4\08212006\J533103.raw

3 <110> APPLICANT: National Institutes of Health  
 4 Bocharov, Alexander  
 5 Baranova, Irina  
 6 Csako, Gyorgy  
 7 Eggerton, Thomas  
 8 Patterson, Amy  
 9 Remaley, Alan  
 10 Vishnyakova, Tatyana  
 12 <120> TITLE OF INVENTION: Scavenger Receptor B1 Targeting for the Treatment of  
 Infection,  
 13 Sepsis and Inflammation  
 15 <130> FILE REFERENCE: 03514.115-PCT  
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/533,103  
 C--> 17 <141> CURRENT FILING DATE: 2005-04-28  
 17 <150> PRIOR APPLICATION NUMBER: 60/422,105  
 18 <151> PRIOR FILING DATE: 2002-10-30  
 20 <160> NUMBER OF SEQ ID NOS: 14  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 21  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 29 <400> SEQUENCE: 1  
 30 gtcttcacca ccatggagaa g 21  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 25  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Homo sapiens  
 38 <400> SEQUENCE: 2  
 39 gcttcaccac cttcttgatg tcatc 25  
 42 <210> SEQ ID NO: 3  
 43 <211> LENGTH: 21  
 44 <212> TYPE: DNA  
 45 <213> ORGANISM: Homo sapiens  
 47 <400> SEQUENCE: 3  
 48 ccacccaacg aaggcttctg c 21  
 51 <210> SEQ ID NO: 4  
 52 <211> LENGTH: 19  
 53 <212> TYPE: DNA  
 54 <213> ORGANISM: Homo sapiens  
 56 <400> SEQUENCE: 4  
 57 ctgaatggcc tccttatcc 19  
 60 <210> SEQ ID NO: 5  
 61 <211> LENGTH: 20

Does Not Comply  
 Corrected Diskette Needed  
 (pg. 2-3)

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Input Set : F:\3514 115 ST25.txt

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62 <212> TYPE: DNA  
 63 <213> ORGANISM: Homo sapiens  
 65 <400> SEQUENCE: 5  
 66 caactacaaa gccctctttg 20  
 69 <210> SEQ ID NO: 6  
 70 <211> LENGTH: 20  
 71 <212> TYPE: DNA  
 72 <213> ORGANISM: Homo sapiens  
 74 <400> SEQUENCE: 6  
 75 cttggctggt ctccatgaag 20  
 78 <210> SEQ ID NO: 7  
 79 <211> LENGTH: 18  
 80 <212> TYPE: DNA  
 81 <213> ORGANISM: Homo sapiens  
 83 <400> SEQUENCE: 7  
 84 ctgaaagctc tccacctc  
 87 <210> SEQ ID NO: 8  
 88 <211> LENGTH: 18  
 89 <212> TYPE: DNA  
 90 <213> ORGANISM: Homo sapiens  
 92 <400> SEQUENCE: 8  
 93 gtgctgatgt accagttg  
 96 <210> SEQ ID NO: 9  
 97 <211> LENGTH: 18  
 98 <212> TYPE: PRT  
 99 <213> ORGANISM: Synthetic  
 101 <400> SEQUENCE: 9  
 103 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 104 1 5 10 15  
 107 Ala Phe  
 111 <210> SEQ ID NO: 10  
 112 <211> LENGTH: 37  
 113 <212> TYPE: PRT  
 114 <213> ORGANISM: Synthetic  
 116 <400> SEQUENCE: 10  
 118 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 119 1 5 10 15  
 122 Ala Phe Pro Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys  
 123 20 25 30  
 126 Leu Lys Glu Ala Phe  
 127 35  
 130 <210> SEQ ID NO: 11  
 131 <211> LENGTH: 37  
 132 <212> TYPE: PRT  
 133 <213> ORGANISM: Synthetic  
 136 <220> FEATURE:  
 137 <221> NAME/KEY: MISC\_FEATURE  
 138 <222> LOCATION: (1)..(37)  
 139 <223> OTHER INFORMATION: All residues D-Amino Acid

Invalid Response

Invalid Response

Same error

Per Sequence  
 rules, 2137  
 response has  
 to be  
 either  
 Artificial  
 Unknown  
 or Genus/  
 Species.

See item  
 #10 on  
 error  
 summary  
 sheet.

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Input Set : F:\3514 115 ST25.txt

Output Set: N:\CRF4\08212006\J533103.raw

141 <400> SEQUENCE: 11  
 143 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 144 1 5 10 15  
 147 Ala Phe Pro Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys  
 148 20 25 30  
 151 Leu Lys Glu Ala Phe  
 152 35  
 155 <210> SEQ ID NO: 12  
 156 <211> LENGTH: 37  
 157 <212> TYPE: PRT  
 158 <213> ORGANISM: Synthetic  
 161 <220> FEATURE:  
 162 <221> NAME/KEY: MISC\_FEATURE  
 163 <222> LOCATION: (1)..(37)  
 164 <223> OTHER INFORMATION: All Ala residues are D-Amino Acids  
 166 <400> SEQUENCE: 12  
 168 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 169 1 5 10 15  
 172 Ala Phe Pro Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys  
 173 20 25 30  
 176 Leu Lys Glu Ala Phe  
 177 35  
 180 <210> SEQ ID NO: 13  
 181 <211> LENGTH: 37  
 182 <212> TYPE: PRT  
 183 <213> ORGANISM: Synthetic  
 186 <220> FEATURE:  
 187 <221> NAME/KEY: MISC\_FEATURE  
 188 <222> LOCATION: (1)..(37)  
 189 <223> OTHER INFORMATION: All Tyr and Val are D-Amino Acid Residues  
 191 <400> SEQUENCE: 13  
 193 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 194 1 5 10 15  
 197 Ala Phe Pro Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys  
 198 20 25 30  
 201 Leu Lys Glu Ala Phe  
 202 35  
 205 <210> SEQ ID NO: 14  
 206 <211> LENGTH: 37  
 207 <212> TYPE: PRT  
 208 <213> ORGANISM: Synthetic  
 211 <220> FEATURE:  
 212 <221> NAME/KEY: MISC\_FEATURE  
 213 <222> LOCATION: (1)..(37)  
 214 <223> OTHER INFORMATION: All Asp, Lys and Ala are D-Amino Acid Residues  
 216 <400> SEQUENCE: 14  
 218 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 219 1 5 10 15  
 222 Ala Phe Pro Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys

same errors

See item  
 #10 on  
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 Summary  
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223		20		25	30
226	Leu	Lys	Glu	Ala	Phe
227		35			

**VERIFICATION SUMMARY**

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Input Set : F:\3514 115 ST25.txt

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date